

## Sequence Comparison A

### RESULT 1

US-09-383-586-31  
; Sequence 31, Application US/09383586  
; Patent No. 6242419  
; GENERAL INFORMATION:  
; APPLICANT: Strachan, Lorna  
; APPLICANT: Sleeman, Matthew  
; APPLICANT: Abernethy, Nevin  
; APPLICANT: Onrust, Rene  
; APPLICANT: Kumble, Anand  
; APPLICANT: Murison, Greg  
; TITLE OF INVENTION: Compounds isolated from stromal cells  
; TITLE OF INVENTION: and methods for their use  
; FILE REFERENCE: 11000.1037c1  
; CURRENT APPLICATION NUMBER: US/09/383,586  
; CURRENT FILING DATE: 1999-08-26  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 31  
; LENGTH: 529  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-383-586-31

Query Match 85.2%; Score 2308.5; DB 3; Length 529;  
Best Local Similarity 88.0%; Pred. No. 4.7e-181;  
Matches 431; Conservative 22; Mismatches 26; Indels 11; Gaps 2;

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Qy      1 MTPSPLLLLLLPPLLLGAFPPAAAARGPPKMADKVVPRQVARLGRTVRLQCPVEGDPPPL 60
      || || ||| ||||| | | |||||:||||||| ||||| ||||| ||||| |||||
Db      1 MTRSPALLL----LLLGALPSAEAAARGPPRMADKVVPRQVARLGRTVRLQCPVEGDPPPL 56

Qy     61 TMWTKDGRTIHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLDI 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     57 TMWTKDGRTIHSGWSRFRVLPQGLKVKVEAEDAGVYVCKATNGFGSLSVNYTLIIMDDI 116

Qy    121 SPGKESLGPDSGGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLKCVASGHPRP 180
      ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    117 SPGKESPGPGSGGGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLKCVASGHPRP 176

Qy    181 DITWMKDDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQ 240
      || ||||| || ||:| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    177 DIMWMKDDQTLTHLEASEHRKKKWTLSLKNLKPEDSGKYTCRVSNKAGAINATYKVDVIQ 236

Qy    241 RTRSKPVLGTGHPVNTTVDFGGTTSFQCKVRSVDVKPVIQWLKRVEYGAEGRHNSTIDVGG 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    237 RTRSKPVLGTGHPVNTTVDFGGTTSFQCKVRSVDVKPVIQWLKRVEYGSEGRHNSTIDVGG 296

Qy    301 QKFVVLPTGDVWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVPDPK 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    297 QKFVVLPTGDVWSRPDGSYLNKLLISRARQDDAGMYICLGANTMGYSFRSAFLTVPDPK 356

Qy    361 PPGPPVASSSSATSLFPWPVVIGIPAGAVFILGTLLLWLCAQKKPCTPAPAPPLPGHRPP 420
      |||||:|||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    357 PPGPPMASSSSSTSLFPWPVVIGIPAGAVFILGTVLLWLCAQKKKPCAPASTLPVPGHRPP 416

Qy    421 GTARDRSGDKDLPSLAALSAGPGVGLCEEHGSAPAPQHLLGPGPVAGPKLYPKLYTDIHT 480
      ||:|:||||||| ||:||||| |||||:| | ||||| ||||| |||||
Db    417 GTSRERSGDKDLPSLA-----VGICEEHGSAMAPQHILASGSTAGPKLYPKLYTDVHT 469

Qy    481 HTHTHSHTHS 490
      |||||: ||:
Db    470 HTHTHCTHT 479
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## Sequence Comparison B

### RESULT 2

Q9H4D7

ID Q9H4D7 PRELIMINARY; PRT; 504 AA.  
AC Q9H4D7;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE FGFR-like protein precursor (Fibroblast growth factor receptor  
DE 5).  
GN FGFR1 OR FGFR5.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Cartilage;  
RX PubMed=11031111;  
RA Wiedemann M., Trueb B.;  
RT "Characterization of a novel protein (FGFR1) from human cartilage  
RT related to FGF receptors.";  
RL Genomics 69:275-279(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21167383; PubMed=11267671;  
RA Kim I., Moon S.O., Yu K.H., Kim U.H., Koh G.Y.;  
RT "A novel fibroblast growth factor receptor-5 preferentially expressed  
RT in the pancreas.";  
RL Biochim. Biophys. Acta 1518:152-156(2001).  
DR EMBL; AJ277437; CAC14171.1; -.  
DR EMBL; AF279689; AAK26742.1; -.  
DR GO; GO:0016021; C:integral to membrane; NAS.  
DR GO; GO:0005007; F:fibroblast growth factor receptor activity; NAS.  
DR GO; GO:0001558; P:regulation of cell growth; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig\_c2.  
DR Pfam; PF00047; ig; 3.  
DR SMART; SM00408; IGc2; 2.  
DR PROSITE; PS50835; IG\_LIKE; 3.  
KW Immunoglobulin domain; Receptor; Signal.  
FT SIGNAL 1 17 POTENTIAL.  
SQ SEQUENCE 504 AA; 54567 MW; 16382E57D4276485 CRC64;

Query Match 99.7%; Score 2701; DB 4; Length 504;  
Best Local Similarity 99.8%; Pred. No. 9.3e-206;  
Matches 503; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MTPSPLLLLLLPPLLGAFPAAAAARGPPKMADKVVPRQVARLGRTVRLQCPVEGDPPPL	60
Db	1	MTPSPLLLLLLPPLLGAFPAAAAARGPPKMADKVVPRQVARLGRTVRLQCPVEGDPPPL	60
Qy	61	TMWTKDGRTIHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLDDI	120
Db	61	TMWTKDGRTIHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLDDI	120
Qy	121	SPGKESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLKCVASGHPRP	180
Db	121	SPGKESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLKCVASGHPRP	180
Qy	181	DITWMKDDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQ	240
Db	181	DITWMKDDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQ	240
Qy	241	RTRSKPVLGTGHPVNTTVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGG	300
Db	241	RTRSKPVLGTGHPVNTTVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGG	300
Qy	301	QKFVVLPTGDVWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVPDPK	360

Db	301		QKFVVLPTGDVWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVLPDPK	360
Qy	361	PPGPPVASSSSATSLPWPVVIGIPAGAVFILGTLLLWLCQAQKKPCTPAPAPPLPGHRPP	420	
Db	361		PQGPPVASSSSATSLPWPVVIGIPAGAVFILGTLLLWLCQAQKKPCTPAPAPPLPGHRPP	420
Qy	421	GTARDRSGDKDLPSLAALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTDIHT	480	
Db	421		GTARDRSGDKDLPSLAALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTDIHT	480
Qy	481	HTHTHSHTHSHVEGKVHQHIHYQC	504	
Db	481		HTHTHSHTHSHVEGKVHQHIHYQC	504

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